



# 7

1

## SEQUENCE LISTING

<110> FARWICK, MIKE  
HUTHMACHER, KLAUS  
PFEFFERLE, WALTER

<120> NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE MIKE17 GENE

<130> 21123/280108/MAS

<140> 09/825,293

<141> 2001-04-04

<150> DE 100 47 867.0

<151> 2000-09-27

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1890

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (252)..(1673)

<223> mike17-Gen

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ctttgcgag gtgacacaat tatcccaaca gttgcaccgt aggtgcctaa aaagttcccg 120

gggcggatgt ggcccgaaca cgccgggcac ctggtggcgg cgggctgcgt cgaaaagcga 180

aatcaacaa gtttgcaaca cctcagtgcc aagagtgggt aaggtgatgg tgatcacgct 240

atagttgcgc c atg gga aag aca tat gtg ggg tcc agg ctg cgc caa ctg 290  
Met Gly Lys Thr Tyr Val Gly Ser Arg Leu Arg Gln Leu

1

5

10

cgc cgc gaa aga gac ctg agc cag gca tcc tta gca gca acc ctt ggc 338  
Arg Arg Glu Arg Asp Leu Ser Gln Ala Ser Leu Ala Ala Thr Leu Gly

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tta tct gca agt tat gta aat cag att gag cac gac gta cgc ccg ctc 386  
Leu Ser Ala Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu

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acc gta ccg gtg tta ttg cgc atc acc gag gcg ttc ggc gta gac gca 434  
Thr Val Pro Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala

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acg ttt ttc tcc cgc gac gat gac tcc cgc ctg ctc gcc gag gtc caa 482  
Thr Phe Phe Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln

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70

75

AI  
Cm T

gac gtc atg ctg gac cgg gag atc aat cct gcg aac gtg gag ctg caa 530  
 Asp Val Met Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln  
 80 85 90

gag ctt tgc gag atg gtg tac aac cac ccc caa cta gcg cgc gcg atg 578  
 Glu Leu Ser Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met  
 95 100 105

gtg gaa atg cac cag cgt tac cga aac gtg cgc gat aag ttc tcc atc 626  
 Val Glu Met His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile  
 110 115 120 125

gca gtg gat aat cgc acc aac acg cct gag gaa cgc cgt ccc atc gcg 674  
 Ala Val Asp Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala  
 130 135 140

gag gcc gtg agc atg ccg cac gaa gag gtc cgc gat ttc att tac gcc 722  
 Glu Ala Val Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala  
 145 150 155

cgc caa aac tac ttc gat gcc ctt gac cgc cgc gcc gaa gcc atc gcc 770  
 Arg Gln Asn Tyr Phe Asp Ala Leu Asp Arg Arg Ala Glu Ala Ile Ala  
 160 165 170

gcg caa ctg ggc tgg cag ccg tac gat tcc cgc gcc atg gaa gat tgc 818  
 Ala Gln Leu Gly Trp Gln Pro Tyr Asp Ser Arg Ala Met Glu Asp Ser  
 175 180 185

atc gcc cgc cgc ctg caa atg gat cac gat gtc acc atc acc tcc tcc 866  
 Ile Ala Arg Arg Leu Gln Met Asp His Asp Val Thr Ile Thr Ser Ser  
 190 195 200 205

aaa gag gaa tcc ggc acg ctg cac cac ttc gac ccc gag acg cgt ctg 914  
 Lys Glu Glu Ser Gly Thr Leu His His Phe Asp Pro Glu Thr Arg Leu  
 210 215 220

ctg aca atc cac gca cgc ctc aac ccc ggg caa cgc gcc ttc cgc atg 962  
 Leu Thr Ile His Ala Arg Leu Asn Pro Gly Gln Arg Ala Phe Arg Met  
 225 230 235

gcc acc gaa ctc ggc tac cta gaa gcc aac gac ctc atc gaa ggt atc 1010  
 Ala Thr Glu Leu Gly Tyr Leu Glu Ala Asn Asp Leu Ile Glu Gly Ile  
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gtt gac gac ggc atc tgg tcc acc ccc gaa gcc cgc acc cta gcc atc 1058  
 Val Asp Asp Gly Ile Trp Ser Thr Pro Glu Ala Arg Thr Leu Ala Ile  
 255 260 265

cgc ggt gtg gcc tcc tac ttc gcc gcc gcc gtg atg ctg ccc tac aaa 1106  
 Arg Gly Val Ala Ser Tyr Phe Ala Ala Ala Val Met Leu Pro Tyr Lys  
 270 275 280 285

atc ttc cac tcc gag gcc gaa aaa tcc ggc tac gac atc gag tac cta 1154  
 Ile Phe His Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu  
 290 295 300

A1  
 Cm. x

ggc caa ctc ttt ggc gtg ggc tat gag aca acc gcc cac cgc ttg tcc 1202  
 Gly Gln Leu Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser  
 305 310 315

acc ctg cag cgc ccc aac ctg cgc ggc atc ccc ttt acc ttc gtg cgc 1250  
 Thr Leu Gln Arg Pro Asn Leu Arg Gly Ile Pro Phe Thr Phe Val Arg  
 320 325 330

gtc gac cgc gcc ggc aac atg tcc aaa cgc caa tcc gcc acc ggc ttc 1298  
 Val Asp Arg Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe  
 335 340 345

cac ttc acc cac tac ggc ggc acc tgc ccc ctg tgg aac gtg ttt gaa 1346  
 His Phe Thr His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu  
 350 355 360 365

acc ttc acc aac ccc ggc caa gtg ctc cgc caa ttc gcg caa atg ccc 1394  
 Thr Phe Thr Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro  
 370 375 380

gac gga cgc aac tac ctg tgg atc tca cgc acc gtg cga cac cac gaa 1442  
 Asp Gly Arg Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu  
 385 390 395

gcc cgg ttc ggc gaa gta gac aaa atg ttc gcc atc ggc ctg ggc tgc 1490  
 Ala Arg Phe Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys  
 400 405 410

gaa gcg cgc cac gcc gac cgc act gtg tac tcc cgc ggt ttc aac ctc 1538  
 Glu Ala Arg His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu  
 415 420 425

cag gac ctc tcc acc gcc acc ccc atc ggg tcc ggc tgc cga gtg tgc 1586  
 Gln Asp Leu Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys  
 430 435 440 445

acc cgc gag aac tgc gcg cag cgc gca ttc cca tcc gtc cac ggc cgc 1634  
 Thr Arg Glu Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg  
 450 455 460

atc aac atc gac gcg cac gaa tcc act atc gcg ccg tac taagaaaagg 1683  
 Ile Asn Ile Asp Ala His Glu Ser Thr Ile Ala Pro Tyr  
 465 470

agcttgcttt acgacgcacc ctgcgggggt ggggttttacc ttttatgaat gatcagcaat 1743

atccgcgtaa acaccatcgg tagccagaag aacatcatcc ggggcgataa tcagggacca 1803

cccgcgtcgc cctgcgctga cgtagattcg ctccctggaga attgcagact catccaaaaa 1863

cacgcgggtgc ttgtttcttct gccctat 1890

&lt;210&gt; 2

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

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Cm.1

&lt;400&gt; 2

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 1 5 10 15  
 Arg Asp Leu Ser Gln Ala Ser Leu Ala Ala Thr Leu Gly Leu Ser Ala  
 20 25 30  
 Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu Thr Val Pro  
 35 40 45  
 Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala Thr Phe Phe  
 50 55 60  
 Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln Asp Val Met  
 65 70 75 80  
 Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln Glu Leu Ser  
 85 90 95  
 Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met Val Glu Met  
 100 105 110  
 His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile Ala Val Asp  
 115 120 125  
 Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala Glu Ala Val  
 130 135 140  
 Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala Arg Gln Asn  
 145 150 155 160  
 Tyr Phe Asp Ala Leu Asp Arg Arg Ala Glu Ala Ile Ala Ala Gln Leu  
 165 170 175  
 Gly Trp Gln Pro Tyr Asp Ser Arg Ala Met Glu Asp Ser Ile Ala Arg  
 180 185 190  
 Arg Leu Gln Met Asp His Asp Val Thr Ile Thr Ser Ser Lys Glu Glu  
 195 200 205  
 Ser Gly Thr Leu His His Phe Asp Pro Glu Thr Arg Leu Leu Thr Ile  
 210 215 220  
 His Ala Arg Leu Asn Pro Gly Gln Arg Ala Phe Arg Met Ala Thr Glu  
 225 230 235 240  
 Leu Gly Tyr Leu Glu Ala Asn Asp Leu Ile Glu Gly Ile Val Asp Asp  
 245 250 255  
 Gly Ile Trp Ser Thr Pro Glu Ala Arg Thr Leu Ala Ile Arg Gly Val  
 260 265 270  
 Ala Ser Tyr Phe Ala Ala Ala Val Met Leu Pro Tyr Lys Ile Phe His  
 275 280 285  
 Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu Gly Gln Leu  
 290 295 300

AI  
 Crit

Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser Thr Leu Gln  
305 310 315 320

Arg Pro Asn Leu Arg Gly Ile Pro Phe Thr Phe Val Arg Val Asp Arg  
325 330 335

Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe His Phe Thr  
340 345 350

His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu Thr Phe Thr  
355 360 365

Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro Asp Gly Arg  
370 375 380

Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu Ala Arg Phe  
385 390 395 400

Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys Glu Ala Arg  
405 410 415

His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu Gln Asp Leu  
420 425 430

Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys Thr Arg Glu  
435 440 445

Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg Ile Asn Ile  
450 455 460

Asp Ala His Glu Ser Thr Ile Ala Pro Tyr  
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<212> DNA

<213> Corynebacterium glutamicum

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<223> Primer mikE17-int1

<400> 3

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<213> Corynebacterium glutamicum

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<223> Primer mikE17-int2

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19

AI  
Cmcd.